

REMARKS

Claims 7-9 and 12-21 and 23 are pending. No new matter has been added by way of the present amendment. For instance, claims 7 and 13 have been amended to simply recite “preparing” a mixture of fragmented DNAs. Further, claim 7 has been amended to recite that the nucleic acid amplification uses “amplification primers as supported by the present specification at page 19, lines 14-16. Claims 10 and 11 have been canceled and claim 12 has been amended to recite a mixture of DNAs having an average size range from 0.5 kbp to 2.5 kbp as supported by the present specification at page 15, lines 1-8. Additionally, claim 13 has been placed into independent format. Lastly, claim 23 is supported by originally filed claim 12. Accordingly, no new matter has been added.

In view of the following remarks Applicants respectfully request that the Examiner withdraw all rejections and allow the currently pending claims.

Objections to the Claims

The Examiner has objected to claims 10 and 11 under 37 C.F.R. 1.75(c) for the reasons recited at pages 2-3 of the outstanding Office Action. Applicants respectfully traverse and submit that claims 10 and 11 have been canceled. Thus, this objection is moot. Reconsideration and withdrawal thereof are respectfully requested.

Issues under 35 U.S.C. 112, 2nd paragraph

The Examiner has rejected claims 13-21 under 35 U.S.C. 112, 2nd paragraph for the reasons recited at pages 3 and 4 of the outstanding Office Action. Applicants respectfully traverse.

The Examiner has rejected claim 13 asserting that its dependency upon claim 7 is confusing. Applicants respectfully traverse and submit that claim 13 has been placed into independent format. Accordingly, this rejection is moot. Reconsideration and withdrawal thereof are respectfully requested.

Issues under 35 U.S.C. 112, 1st paragraph

The Examiner has rejected claim 7-21 under 35 U.S.C. 112, 1st paragraph for the reasons recited at pages 4-7 of the outstanding Office Action. In particular, the Examiner asserts that the specification, while being enabling for a hydrodynamic point-sink shearing method, is not enabling for a “any” fragmentation method. Applicants respectfully traverse. Applicants point out that the present claims, for instance, independent claim 7 and independent claim 13, do not recite “DNA fragmentation means”.

The present invention essentially relates to preparation of a genomic DNA library maintaining copy numbers of a set of genes or sequences on the genomic DNA and an abundance ratio of the set of genes or sequences on the genomic DNA, and is not characterized by the method of DNA fragmentation. That is, despite the method of DNA fragmentation, the genomic DNA library of the present invention can be produced by using a mixture of fragmented

DNAs having distribution ratio of 1 to 5 and having a size convergence rate of 80% or more. The method for preparing the fragmented DNAs is specifically described at page 15, line 1 to page 16, line 25 of the present specification as originally filed. Also, methods for evaluation of the distribution ratio and the size convergence rate are disclosed at page 4, lines 4-25 of the present specification. Accordingly, a person skilled in the art can prepare and evaluate the fragmented DNAs having the above-mentioned features so as to produce the genomic DNA library of the present invention. Accordingly, the Examiner is respectfully requested to withdraw this rejection.

However, Applicants further point out that even without the amendments to remove the “means-plus-function” language, the scope of the “fragmentation means” would not have referred to “any” fragmentation means as asserted by the Examiner. Rather, claims reciting “means-plus-function” elements must be construed in accordance with 35 U.S.C. § 112, sixth paragraph (section 112(6)), which reads:

An element in a claim for a combination may be expressed as a means or step for performing a specified function without the recital of structure, material, or acts in support thereof, and such claim shall be construed to cover the corresponding structure, material, or acts described in the specification and equivalents thereof.

Pursuant to 35 U.S.C. § 112, sixth paragraph, means-plus-function limitations are interpreted according to structures disclosed in the specification (which achieve identical function) and equivalent structures thereof. However, since the present claims are fully supported, this issue is moot.

Thus, the recitation of the means-plus-function in the claims does not relate to "any fragmentation means", rather, it relates to structures which achieve identical function disclosed in the specification and equivalent structures thereof.

Issues under 35 U.S.C. 102(b)

The Examiner has rejected claims 7-12 under 35 U.S.C. § 102(b) as being anticipated by Oefner et al., Nucleic Acids Research, 1996, Vol. 24, No. 20, pages 3879-3886 (hereinafter referred to as Oefner). Applicants respectfully traverse.

Oefner discloses the production of transformants by subcloning fragmented genomic DNA to a plasmid vector so that the subcloning efficiency of each clone and the proliferation efficiency of each transformant differs from one another. Further, mutations such as homologous recombination, omission and substitution may occur upon reproduction in a host cell. In the case where the fragmented DNA contains a harmful sequence to the host, a subclone cannot be obtained. Accordingly, according to the method of Oefner, a genomic DNA library maintaining copy numbers of a set of genes or sequences on the genomic DNA and an abundance ratio of the set of genes or sequences on the genomic DNA cannot be produced. Further, in order to produce the DNA library comprising a lot of fragmented DNAs, subcloning of each clone and incubation of each transformant are necessary and purification of DNA therefrom, thus, incubated transformants are also necessary. As such, an enormous amount of work is required.

In contrast, the method of the present invention is characterized in that a genomic DNA library maintaining copy numbers of a set of genes or sequences on the genomic DNA and an abundance ratio of the set of genes or sequences on the genomic DNA can be produced. That is, even if many identical or similar sequences such as microsatellites or superfamilies of genes exist in the genome, a DNA library maintaining the copy numbers and the abundance ratio can be obtained in the present invention. In addition, by the method of the present invention, fragmented DNAs as a mixture can be amplified in an *in vitro* reaction system such that the production is very simple.

Accordingly, Applicants respectfully submit that there is no anticipation based upon Oefner. Reconsideration and withdrawal of this rejection are therefore respectfully requested.

Issues under 35 U.S.C. 103(a)

The Examiner has rejected claims 7-16 under 35 U.S.C. § 103(a) as being obvious over Oefner in view of Lucito et al., PNAS, 1998, Vol. 95, pages 4487-4492 (hereinafter referred to as Lucito).

The Examiner has also rejected claims 17-21 under 35 U.S.C. § 103(a) as being obvious over Oefner in view of Lucito and Sorge et al., USP 5,556,772.

Applicants respectfully traverse each of the above rejections.

Deficiencies with respect to Oefner are noted above. The secondary references are unable to cure these deficiencies.

In Lucito, there is disclosed a genomic DNA that is cleaved by restriction enzyme. Further adaptors are ligated to the obtained DNA fragments, followed by carrying out PCR to provide a library.

In contrast, the present invention is characterized by a method of preparing a genomic DNA library maintaining copy numbers of a set of genes or sequences on the genomic DNA and an abundance ratio of the set of genes or sequences on the genomic DNA where the fragmented genomic DNAs are compositionally unchanged after repeated amplifications. That is, the present invention has the excellent feature in that even after repeated amplifications, fragmented DNAs are uniformly amplified and retain the original abundance ratio, i.e. there is retained a large number of fragmented DNAs as they originally were and also a small number of fragmented DNAs as they originally were.

In Oefner, a fragmentation method is disclosed such that more than 90% of the fragments exist within a 2-fold size distribution. However, Oefner and Lucito fail to teach or suggest distribution ratio, abundance ratio and compositional aspect of each fragmented genomic DNA in amplification of nucleic acids. As such, even if these references were combined, only a genomic DNA library having the same size can be produced, and the feature of the present invention, i.e., maintaining the copy numbers and the abundance ratio cannot be achieved.

Further, the Examiner refers to Sorge as a secondary reference with respect to claims 17 to 21. However, these claims are dependent claims from claim 13 for which grounds of rejections are overcome as noted above. Also, Sorge cannot cure the deficiencies of the other references.

Accordingly, Applicants respectfully submit that the cited art, whether taken individually or in combination, fail to render the present claims obvious. Accordingly, the Examiner is respectfully requested to withdraw these rejections.


Should there be any outstanding matters that need to be resolved in the present application, the Examiner is respectfully requested to contact Craig A. McRobbie (Reg. No. 42,874) at the telephone number of the undersigned below, to conduct an interview in an effort to expedite prosecution in connection with the present application.

Pursuant to the provisions of 37 C.F.R. §§ 1.17 and 1.136(a), the Applicants hereby petition for an extension of two (2) months to August 22, 2005, in which to file a reply to the Office Action. The required fee of \$450.00 is enclosed herewith.

If necessary, the Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 02-2448 for any additional fees required under 37 C.F.R. §§ 1.16 or 1.17; particularly, extension of time fees.

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Respectfully submitted,

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